

GENERAL PATHWAY OF LIGNIN BIOSYNTHESIS

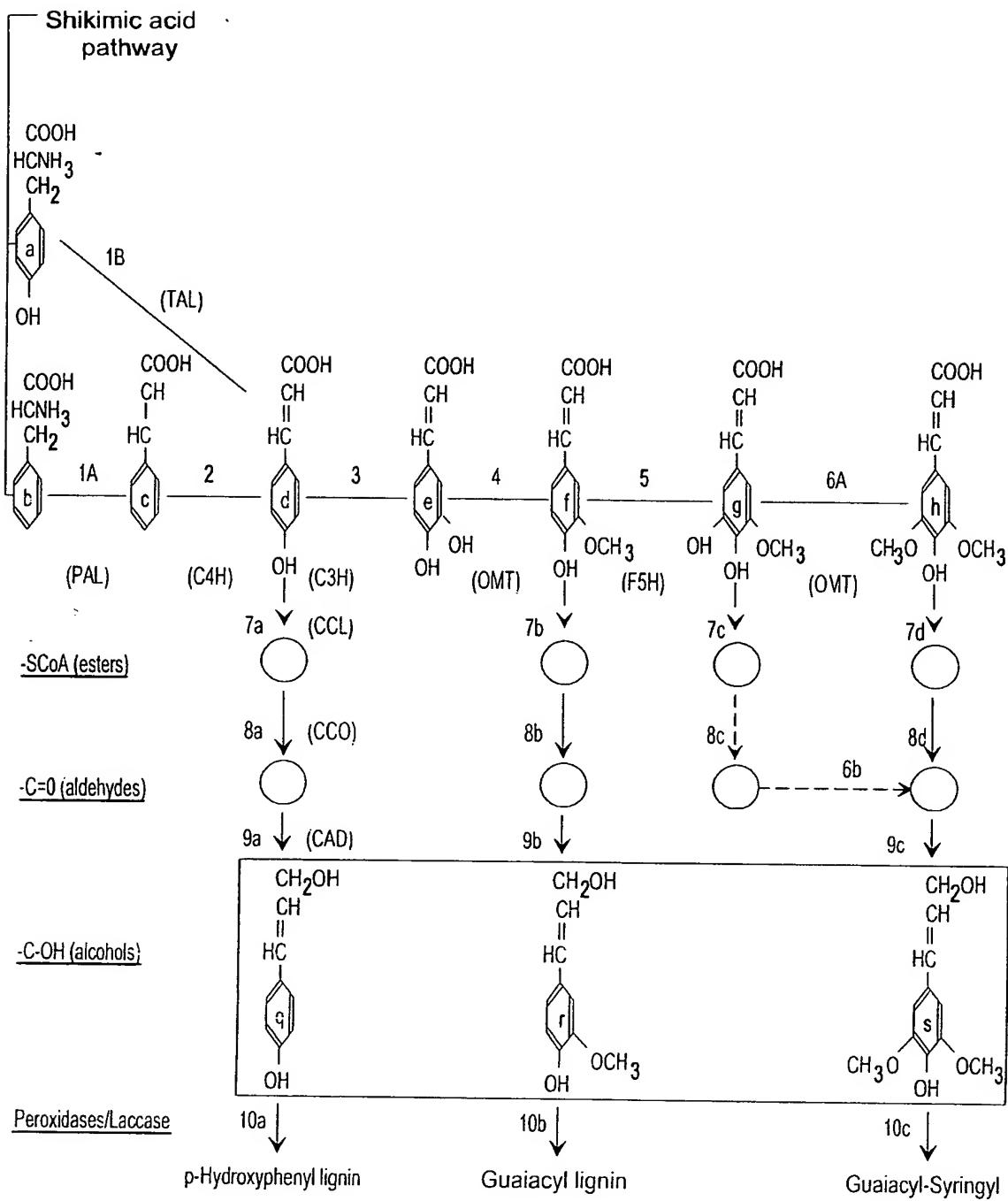


FIG. 1

SEQ ID 5

<400> 5
 cggcacgagc cctacccctt ttcttgaaa aattccccca ttcgatcaca atccgggcct 60
 caaaaa atg gga tca aca agc gaa acg aag atg agc ccg agt gaa gca 108
 Met Gly Ser Thr Ser Glu Thr Lys Met Ser Pro Ser Glu Ala
 1 5 10
 gca gca gca gaa gaa gca ttc gta ttc gct atg caa tta acc agt 156
 Ala Ala Ala Glu Glu Ala Phe Val Phe Ala Met Gln Leu Thr Ser
 15 20 25 30
 gct tca gtt ctt ccc atg gtc cta aaa tca gcc ata gag ctc gac gtc 204
 Ala Ser Val Leu Pro Met Val Leu Lys Ser Ala Ile Glu Leu Asp Val
 35 40 45
 tta gaa atc atg gct aaa gct ggt cca ggt gcg cac ata tcc aca tct 252
 Leu Glu Ile Met Ala Lys Ala Gly Pro Gly Ala His Ile Ser Thr Ser
 50 55 60
 gac ata gcc tct aag ctg ccc aca aag aat cca gat gca gcc gtc atg 300
 Asp Ile Ala Ser Lys Leu Pro Thr Lys Asn Pro Asp Ala Ala Val Met
 65 70 75
 ctt gac cgt atg ctc cgc ctc ttg gct agc tac tct gtt cta acg tgc 348
 Leu Asp Arg Met Leu Arg Leu Leu Ala Ser Tyr Ser Val Leu Thr Cys
 80 85 90
 tct ctc cgc acc ctc cct gac ggc aag atc gag agg ctt tac ggc ctt 396
 Ser Leu Arg Thr Leu Pro Asp Gly Lys Ile Glu Arg Leu Tyr Gly Leu
 95 100 105 110
 gca ccc gtt tgt aaa ttc ttg acc aga aac gat gat gga gtc tcc ata 444
 Ala Pro Val Cys Lys Phe Leu Thr Arg Asn Asp Asp Gly Val Ser Ile
 115 120 125
 gcc gct ctg tct ctc atg aat caa gac aag gtc ctc atg gag agc tgg 492
 Ala Ala Leu Ser Leu Met Asn Gln Asp Lys Val Leu Met Glu Ser Trp
 130 135 140
 tac cac ttg acc gag gca gtt ctt gaa ggt gga att cca ttt aac aag 540
 Tyr His Leu Thr Glu Ala Val Leu Glu Gly Gly Ile Pro Phe Asn Lys
 145 150 155

Fig. 2A

SEQ ID 5

gcc tat gga atg aca gca ttt gag tac cat ggc acc gat ccc aga ttc		588
Ala Tyr Gly Met Thr Ala Phe Glu Tyr His Gly Thr Asp Pro Arg Phe		
160	165	170
aac aca gtt ttc aac aat gga atg tcc aat cat tcg acc att acc atg		636
Asn Thr Val Phe Asn Asn Gly Met Ser Asn His Ser Thr Ile Thr Met		
175	180	185
aag aaa atc ctt gag act tac aaa ggg ttc gag gga ctt gga tct gtg		684
Lys Lys Ile Leu Glu Thr Tyr Lys Gly Phe Glu Gly Leu Gly Ser Val		
195	200	205
gtt gat gtt ggt ggt ggc act ggt gcc cac ctt aac atg att atc gct		732
Val Asp Val Gly Gly Thr Gly Ala His Leu Asn Met Ile Ile Ala		
210	215	220
aaa tac ccc atg atc aag ggc att aac ttc gac ttg cct cat gtt att		780
Lys Tyr Pro Met Ile Lys Gly Ile Asn Phe Asp Leu Pro His Val Ile		
225	230	235
gag gag gct ccc tcc tat cct ggt gtg gag cat gtt ggt gga gat atg		828
Glu Glu Ala Pro Ser Tyr Pro Gly Val Glu His Val Gly Gly Asp Met		
240	245	250
ttt gtt agt gtt cca aaa gga gat gcc att ttc atg aag tgg ata tgt		876
Phe Val Ser Val Pro Lys Gly Asp Ala Ile Phe Met Lys Trp Ile Cys		
255	260	265
cat gat tgg agc gat gaa cac tgc ttg aag ttt ttg aag aaa tgt tat		924
His Asp Trp Ser Asp Glu His Cys Leu Lys Phe Leu Lys Lys Cys Tyr		
275	280	285
gaa gca ctt cca acc aat ggg aag gtg atc ctt gct gaa tgc atc ctc		972
Glu Ala Leu Pro Thr Asn Gly Lys Val Ile Leu Ala Glu Cys Ile Leu		
290	295	300
ccc gtg gcg cca gac gca agc ctc ccc act aag gca gtg gtc cat att		1020
Pro Val Ala Pro Asp Ala Ser Leu Pro Thr Lys Ala Val Val His Ile		
305	310	315
gat gtc atc atg ttg gct cat aac cca ggt ggg aaa gag aga act gag		1068
Asp Val Ile Met Leu Ala His Asn Pro Gly Gly Lys Glu Arg Thr Glu		
320	325	330
aag gag ttt gag gcc ttg gcc aag ggg gct gga ttt gaa ggt ttc cga		1116
Lys Glu Phe Glu Ala Leu Ala Lys Gly Ala Gly Phe Glu Gly Phe Arg		

Fig. 2B

SEQ ID 5

335	340	345	350	
gt` gta gcc tcg tgc gct tac aat aca tgg atc atc gaa ttt ttg aag				1164
Val Val Ala Ser Cys Ala Tyr Asn Thr Trp Ile Ile Glu Phe Leu Lys				
355	360	365		
aag att` tgagtcctta ctggccttg agtacataat accaactcct ttgggtttc				1220
Lys Ile				
gagattgtga ttgtgattgt gattgtctct ctttcgcagt tggccttatg atataatgta				1280
tcgttaactc gatcacagaaa gtcggaaaaga cagtgaatgt acactgcttt ataaaataaaa				1340
aattttaaga ttttggattca tgaaaaaaaaaaaaaaaaaaaaaaa				1380

Fig. 2C

SEQ ID 6

<400> 6
Met Gly Ser Thr Ser Glu Thr Lys Met Ser Pro Ser Glu Ala Ala Ala
1 5 10 15

Ala Glu Glu Glu Ala Phe Val Phe Ala Met Gln Leu Thr Ser Ala Ser
20 25 30

Val Leu Pro Met Val Leu Lys Ser Ala Ile Glu Leu Asp Val Leu Glu
35 40 45

Ile Met Ala Lys Ala Gly Pro Gly Ala His Ile Ser Thr Ser Asp Ile
50 55 60

Ala Ser Lys Leu Pro Thr Lys Asn Pro Asp Ala Ala Val Met Leu Asp
65 70 75 80

Arg Met Leu Arg Leu Leu Ala Ser Tyr Ser Val Leu Thr Cys Ser Leu
85 90 95

Arg Thr Leu Pro Asp Gly Lys Ile Glu Arg Leu Tyr Gly Leu Ala Pro
100 105 110

Val Cys Lys Phe Leu Thr Arg Asn Asp Asp Gly Val Ser Ile Ala Ala
115 120 125

Leu Ser Leu Met Asn Gln Asp Lys Val Leu Met Glu Ser Trp Tyr His
130 135 140

Leu Thr Glu Ala Val Leu Glu Gly Ile Pro Phe Asn Lys Ala Tyr
145 150 155 160

Gly Met Thr Ala Phe Glu Tyr His Gly Thr Asp Pro Arg Phe Asn Thr
165 170 175

Val Phe Asn Asn Gly Met Ser Asn His Ser Thr Ile Thr Met Lys Lys
180 185 190

Ile Leu Glu Thr Tyr Lys Gly Phe Glu Gly Leu Gly Ser Val Val Asp
195 200 205

Val Gly Gly Gly Thr Gly Ala His Leu Asn Met Ile Ile Ala Lys Tyr
210 215 220

Pro Met Ile Lys Gly Ile Asn Phe Asp Leu Pro His Val Ile Glu Glu
225 230 235 240

Fig. 2D

SEQ ID 6

Ala Pro Ser Tyr Pro Gly Val Glu His Val Gly Gly Asp Met Phe Val
245 250 255

Ser Val Pro Lys Gly Asp Ala Ile Phe Met Lys Trp Ile Cys His Asp
260 265 270

Trp Ser Asp Glu His Cys Leu Lys Phe Leu Lys Lys Cys Tyr Glu Ala
275 280 285

Leu Pro Thr Asn Gly Lys Val Ile Leu Ala Glu Cys Ile Leu Pro Val
290 295 300

Ala Pro Asp Ala Ser Leu Pro Thr Lys Ala Val Val His Ile Asp Val
305 310 315 320

Ile Met Leu Ala His Asn Pro Gly Gly Lys Glu Arg Thr Glu Lys Glu
325 330 335

Phe Glu Ala Leu Ala Lys Gly Ala Gly Phe Glu Gly Phe Arg Val Val
340 345 350

Ala Ser Cys Ala Tyr Asn Thr Trp Ile Ile Glu Phe Leu Lys Lys Ile
355 360 365

Fig. 2E

SEQ ID 7

<400> 7

cggcacgagc tcattttcca cttctggttt gatctctgca attcttccat cagtcctta 59

atg gag acc caa aca aaa caa gaa gaa atc ata tat cgg tcg aaa ctc 107
 Met Glu Thr Gln Thr Lys Gln Glu Glu Ile Ile Tyr Arg Ser Lys Leu
 1 5 10 15

ccc gat atc tac atc ccc aaa cac ctc cct tta cat tcg tat tgt ttc 155
 Pro Asp Ile Tyr Ile Pro Lys His Leu Pro Leu His Ser Tyr Cys Phe
 20 25 30

gag aac atc tca cag ttc ggc tcc cgc ccc tgt ctg atc aat ggc gca 203
 Glu Asn Ile Ser Gln Phe Gly Ser Arg Pro Cys Leu Ile Asn Gly Ala
 35 40 45

acg ggc aag tat tac aca tat gct gag gtt gag ctc att gcg cgc aag 251
 Thr Gly Lys Tyr Tyr Thr Ala Glu Val Glu Leu Ile Ala Arg Lys
 50 55 60

gtc gca tcc ggc ctc aac aaa ctc ggc gtt cga caa ggt gac atc atc 299
 Val Ala Ser Gly Leu Asn Lys Leu Gly Val Arg Gln Gly Asp Ile Ile
 65 70 75 80

atg ctt ttg cta ccc aac tcg ccg gag ttc gtg ttt tca att ctc ggc 347
 Met Leu Leu Leu Pro Asn Ser Pro Glu Phe Val Phe Ser Ile Leu Gly
 85 90 95

gca tcc tac cgc ggg gct gcc gcc acc gca aac ccg ttt tat acc 395
 Ala Ser Tyr Arg Gly Ala Ala Ala Thr Ala Ala Asn Pro Phe Tyr Thr
 100 105 110

cct gcc gag atc agg aag caa gcc aaa acc tcc aac gcc agg ctt att 443
 Pro Ala Glu Ile Arg Lys Gln Ala Lys Thr Ser Asn Ala Arg Leu Ile
 115 120 125

atc aca cat gcc tgt tac tat gag aaa gtg aag gac ttg gtg gaa gag 491
 Ile Thr His Ala Cys Tyr Tyr Glu Lys Val Lys Asp Leu Val Glu Glu
 130 135 140

aac gtt gcc aag atc ata tgt ata gac tca ccc ccg gac ggt tgt ttg 539
 Asn Val Ala Lys Ile Ile Cys Ile Asp Ser Pro Pro Asp Gly Cys Leu
 145 150 155 160

Fig. 3A

SEQ ID 7

cac ttc tcg g ^{tg} ctg agt gag g ^{cg} gac gag aac gac atg ccc aat gta	587		
His Phe Ser Glu Leu Ser Glu Ala Asp Glu Asn Asp Met Pro Asn Val			
165	170	175	
gag att gac ccc gat gat g ^{tg} g ^{tg} g ^{cg} ctg ccg tac tcg tca g ^{gg} acg	635		
Glu Ile Asp Pro Asp Asp Val Val Ala Leu Pro Tyr Ser Ser Gly Thr			
180	185	190	
acg ggt tta cca aag g ^{gg} g ^{tg} atg cta aca cac aag gga caa g ^{tg} acg	683		
Thr Gly Leu Pro Lys Gly Val Met Leu Thr His Lys Gly Gln Val Thr			
195	200	205	
agt g ^{tg} g ^{cg} caa cag g ^{tg} gac g ^{gg} gag aat ccg aac ctg tat ata cat	731		
Ser Val Ala Gln Gln Val Asp Gly Glu Asn Pro Asn Leu Tyr Ile His			
210	215	220	
agc gag gac g ^{tg} gtt ctg tgc g ^{tg} ttg cct ctg ttt cac atc tac tcg	779		
Ser Glu Asp Val Val Leu Cys Val Leu Pro Leu Phe His Ile Tyr Ser			
225	230	235	240
atg aac gtc atg ttt tgc g ^{gg} tta cga gtt g ^{gt} g ^{cg} g ^{cg} att ctg att	827		
Met Asn Val Met Phe Cys Gly Leu Arg Val Gly Ala Ala Ile Leu Ile			
245	250	255	
atg cag aaa ttt gaa ata tat g ^{gg} ttg tta gag ctg gtc aga agt aca	875		
Met Gln Lys Phe Glu Ile Tyr Gly Leu Leu Glu Leu Val Arg Ser Thr			
260	265	270	
g ^{gt} gac cat cat gcc tat cgt aca ccc atc gta ttg gca atc tcc aag	923		
Gly Asp His His Ala Tyr Arg Thr Pro Ile Val Leu Ala Ile Ser Lys			
275	280	285	
act ccg gat ctt cac aac tat gat g ^{tg} tcc tcc att cgg act gtc atg	971		
Thr Pro Asp Leu His Asn Tyr Asp Val Ser Ser Ile Arg Thr Val Met			
290	295	300	
tca g ^{gt} g ^{cg} g ^{ct} ctg g ^{gc} aag gaa ctt gaa gat tct gtc aga g ^{ct}	1019		
Ser Gly Ala Ala Pro Leu Gly Lys Glu Leu Glu Asp Ser Val Arg Ala			
305	310	315	320
aag ttt ccc acc gcc aaa ctt g ^{gt} cag g ^{ga} tat g ^{ga} atg acg gag g ^{ca}	1067		
Lys Phe Pro Thr Ala Lys Leu Gly Gln Gly Tyr Gly Met Thr Glu Ala			
325	330	335	
ggg ccc g ^{tg} cta g ^{cg} atg t ^{gt} ttg g ^{ca} ttt g ^{cc} aag gaa g ^{gg} ttt gaa	1115		
Gly Pro Val Leu Ala Met Cys Leu Ala Phe Ala Lys Glu Gly Phe Glu			
340	345	350	

Fig. 3B

SEQ ID 7

ata aaa tcg ggg gca tct gga act gtt tta agg aac gca cag atg aag		1163
Ile Lys Ser Gly Ala Ser Gly Thr Val Leu Arg Asn Ala Gln Met Lys		
355	360	365
att gtg gac cct gaa acc ggt gtc act ctc cct cga aac caa ccc gga		1211
Ile Val Asp Pro Glu Thr Gly Val Thr Leu Pro Arg Asn Gln Pro Gly		
370	375	380
gag att tgc att aga gga gac caa atc atg aaa ggt tat ctt aat gat		1259
Glu Ile Cys Ile Arg Gly Asp Gln Ile Met Lys Gly Tyr Leu Asn Asp		
385	390	395
395	400	
cct gag gcg acc gag aga acc ata gac aag gaa ggt tgg tta cac aca		1307
Pro Glu Ala Thr Glu Arg Thr Ile Asp Lys Glu Gly Trp Leu His Thr		
405	410	415
ggt gat gtg ggc tac atc gac gat gac act gag ctc ttc att gtt gat		1355
Gly Asp Val Gly Tyr Ile Asp Asp Asp Thr Glu Leu Phe Ile Val Asp		
420	425	430
cgg ttg aag gaa ctg atc aaa tac aaa ggg ttt cag gtg gca ccc gct		1403
Arg Leu Lys Glu Leu Ile Lys Tyr Lys Gly Phe Gln Val Ala Pro Ala		
435	440	445
gag ctt gag gcc atg ctc ctc aac cat ccc aac atc tct gat gct gcc		1451
Glu Leu Glu Ala Met Leu Leu Asn His Pro Asn Ile Ser Asp Ala Ala		
450	455	460
460		
gtc gtc cca atg aaa gac gat gaa gct gga gag ctc cct gtg gcg ttt		1499
Val Val Pro Met Lys Asp Asp Glu Ala Gly Glu Leu Pro Val Ala Phe		
465	470	475
475	480	
gtt gta aga tca gat ggt tct cag ata tcc gag gct gaa atc agg caa		1547
Val Val Arg Ser Asp Gly Ser Gln Ile Ser Glu Ala Glu Ile Arg Gln		
485	490	495
495		
tac atc gca aaa cag gtg gtt ttt tat aaa aga ata cat cgc gta ttt		1595
Tyr Ile Ala Lys Gln Val Val Phe Tyr Lys Arg Ile His Arg Val Phe		
500	505	510
510		
ttc gtc gaa gcc att cct aaa gcg ccc tct ggc aaa atc ttg cg aag		1643
Phe Val Glu Ala Ile Pro Lys Ala Pro Ser Gly Lys Ile Leu Arg Lys		
515	520	525
525		
gac ctg aga gcc aaa ttg gcg tct ggt ctt ccc aat taattctcat		1689
Asp Leu Arg Ala Lys Leu Ala Ser Gly Leu Pro Asn		
530	535	540

Fig. 3C

SEQ ID 7

tcgctaccct cctttctctt atcatacgcc aacacgaacg aagaggctca attaaacgct 1749
gctcattcga agcggctcaa ttaaagctgc tcattcatgt ccaccgagtg ggcagcctgt 1809
cttggggta tttttttca tttgattcag ctgtgagaag ccagaccctc attatttatt 1869
gtgaaattca caagaatgtc tgtaaatcga tgtttgaggt gatgggttc aaaacactt 1929
tgacattgtt tacgttgtat ttctgtgt tgaaaataac tactttgtat gactttatt 1989
tggaaagata acctttcaaa aaaaaaaaaa aaaaaa 2025

Fig. 3D

SEQ ID 8

<400> 8

Met Glu Thr Gln Thr Lys Gln Glu Glu Ile Ile Tyr Arg Ser Lys Leu
1 5 10 15

Pro Asp Ile Tyr Ile Pro Lys His Leu Pro Leu His Ser Tyr Cys Phe
20 25 30

Glu Asn Ile Ser Gln Phe Gly Ser Arg Pro Cys Leu Ile Asn Gly Ala
35 40 45

Thr Gly Lys Tyr Tyr Thr Tyr Ala Glu Val Glu Leu Ile Ala Arg Lys
50 55 60

Val Ala Ser Gly Leu Asn Lys Leu Gly Val Arg Gln Gly Asp Ile Ile
65 70 75 80

Met Leu Leu Leu Pro Asn Ser Pro Glu Phe Val Phe Ser Ile Leu Gly
85 90 95

Ala Ser Tyr Arg Gly Ala Ala Ala Thr Ala Ala Asn Pro Phe Tyr Thr
100 105 110

Pro Ala Glu Ile Arg Lys Gln Ala Lys Thr Ser Asn Ala Arg Leu Ile
115 120 125

Ile Thr His Ala Cys Tyr Tyr Glu Lys Val Lys Asp Leu Val Glu Glu
130 135 140

Asn Val Ala Lys Ile Ile Cys Ile Asp Ser Pro Pro Asp Gly Cys Leu
145 150 155 160

His Phe Ser Glu Leu Ser Glu Ala Asp Glu Asn Asp Met Pro Asn Val
165 170 175

Glu Ile Asp Pro Asp Asp Val Val Ala Leu Pro Tyr Ser Ser Gly Thr
180 185 190

Thr Gly Leu Pro Lys Gly Val Met Leu Thr His Lys Gly Gln Val Thr
195 200 205

Ser Val Ala Gln Gln Val Asp Gly Glu Asn Pro Asn Leu Tyr Ile His
210 215 220

Ser Glu Asp Val Val Leu Cys Val Leu Pro Leu Phe His Ile Tyr Ser
225 230 235 240

SEQ ID 8

Met Asn Val Met Phe Cys Gly Leu Arg Val Gly Ala Ala Ile Leu Ile
245 250 255

Met Gln Lys Phe Glu Ile Tyr Gly Leu Leu Glu Leu Val Arg Ser Thr
260 265 270

Gly Asp His His Ala Tyr Arg Thr Pro Ile Val Leu Ala Ile Ser Lys
275 280 285

Thr Pro Asp Leu His Asn Tyr Asp Val Ser Ser Ile Arg Thr Val Met
290 295 300

Ser Gly Ala Ala Pro Leu Gly Lys Glu Leu Glu Asp Ser Val Arg Ala
305 310 315 320

Lys Phe Pro Thr Ala Lys Leu Gly Gln Gly Tyr Gly Met Thr Glu Ala
325 330 335

Gly Pro Val Leu Ala Met Cys Leu Ala Phe Ala Lys Glu Gly Phe Glu
340 345 350

Ile Lys Ser Gly Ala Ser Gly Thr Val Leu Arg Asn Ala Gln Met Lys
355 360 365

Ile Val Asp Pro Glu Thr Gly Val Thr Leu Pro Arg Asn Gln Pro Gly
370 375 380

Glu Ile Cys Ile Arg Gly Asp Gln Ile Met Lys Gly Tyr Leu Asn Asp
385 390 395 400

Pro Glu Ala Thr Glu Arg Thr Ile Asp Lys Glu Gly Trp Leu His Thr
405 410 415

Gly Asp Val Gly Tyr Ile Asp Asp Asp Thr Glu Leu Phe Ile Val Asp
420 425 430

Arg Leu Lys Glu Leu Ile Lys Tyr Lys Gly Phe Gln Val Ala Pro Ala
435 440 445

Glu Leu Glu Ala Met Leu Leu Asn His Pro Asn Ile Ser Asp Ala Ala
450 455 460

Val Val Pro Met Lys Asp Asp Glu Ala Gly Glu Leu Pro Val Ala Phe
465 470 475 480

Fig. 3F

SEQ ID 8

Val Val Arg Ser Asp Gly Ser Gln Ile Ser Glu Ala Glu Ile Arg Gln
485 490 495

Tyr Ile Ala Lys Gln Val Val Phe Tyr Lys Arg Ile His Arg Val Phe
500 505 510

Phe Val Glu Ala Ile Pro Lys Ile Pro Ser Gly Lys Ile Leu Arg Lys
515 520 525

Asp Leu Arg Ala Lys Leu Ala Ser Gly Leu Pro Asn
530 535 540

Fig. 3G

SEQ ID 1

cggcacgagg aaaccctaaa actcacctct cttacccttt ctcttca atg gct ttc 56
 Met Ala Phe
 1

ctt cta ata ccc atc tca ata atc ttc atc gtc tta gct tac cag ctc 104
 Leu Leu Ile Pro Ile Ser Ile Ile Phe Ile Val Leu Ala Tyr Gln Leu
 5 - 10 15

tat caa cgg ctc aga ttt aag ctc cca ccc ggc cca cgt cca tgg ccg 152
 Tyr Gln Arg Leu Arg Phe Lys Leu Pro Pro Gly Pro Arg Pro Trp Pro
 20 25 30 35

atc gtc gga aac ctt tac gac ata aaa ccg gtg agg ttc cgg tgt ttc 200
 Ile Val Gly Asn Leu Tyr Asp Ile Lys Pro Val Arg Phe Arg Cys Phe
 40 45 50

gcc gag tgg tca caa gcg tac ggt ccg atc ata tcg gtg tgg ttc ggt 248
 Ala Glu Trp Ser Gln Ala Tyr Gly Pro Ile Ile Ser Val Trp Phe Gly
 55 60 65

tca acg ttg aat gtg atc gta tcg aat tcg gaa ttg gct aag gaa gtg 296
 Ser Thr Leu Asn Val Ile Val Ser Asn Ser Glu Leu Ala Lys Glu Val
 70 75 80

ctc aag gaa aaa gat caa caa ttg gct gat agg cat agg agt aga tca 344
 Leu Lys Glu Lys Asp Gln Gln Leu Ala Asp Arg His Arg Ser Arg Ser
 85 90 95

gct gcc aaa ttt agc agg gat ggg cag gac ctt ata tgg gct gat tat 392
 Ala Ala Lys Phe Ser Arg Asp Gly Gln Asp Leu Ile Trp Ala Asp Tyr
 100 105 110 115

gga cct cac tat gtg aag gtt aca aag gtt tgt acc ctc gag ctt ttt 440
 Gly Pro His Tyr Val Lys Val Thr Lys Val Cys Thr Leu Glu Leu Phe
 120 125 130

act cca aag cgg ctt gaa gct ctt aga ccc att aga gaa gat gaa gtt 488
 Thr Pro Lys Arg Leu Glu Ala Leu Arg Pro Ile Arg Glu Asp Glu Val
 135 140 145

aca gcc atg gtt gag tcc att ttt aat gac act gcg aat cct gaa aat 536
 Thr Ala Met Val Glu Ser Ile Phe Asn Asp Thr Ala Asn Pro Glu Asn
 150 155 160

Fig. 4A

SEQ ID 1

tat	ggg	aag	agt	atg	ctg	gtg	aag	aag	tat	ttg	gga	gca	gta	gca	ttc	584
Tyr	Gly	Lys	Ser	Met	Leu	Val	Lys	Lys	Tyr	Leu	Gly	Ala	Val	Ala	Phe	
165					170					175						
aac	aac	att	aca	aga	ctc	gca	ttt	gga	aag	cga	ttc	gtg	aat	tca	gag	632
Asn	Asn	Ile	Thr	Arg	Leu	Ala	Phe	Gly	Lys	Arg	Phe	Val	Asn	Ser	Glu	
180	-		185						190				195			
ggt	gta	atg	gac	gag	caa	gga	ctt	gaa	ttt	aag	gaa	att	gtg	gcc	aat	680
Gly	Val	Met	Asp	Glu	Gln	Gly	Leu	Glu	Phe	Lys	Glu	Ile	Val	Ala	Asn	
							200			205			210			
gga	ctc	aag	ctt	ggt	gcc	tca	ctt	gca	atg	gct	gag	cac	att	cct	tgg	728
Gly	Leu	Lys	Leu	Gly	Ala	Ser	Leu	Ala	Met	Ala	Glu	His	Ile	Pro	Trp	
							215			220			225			
ctc	cgt	tgg	atg	ttc	cca	ctt	gag	gaa	ggg	gcc	ttt	gcc	aag	cat	ggg	776
Leu	Arg	Trp	Met	Phe	Pro	Leu	Glu	Glu	Gly	Ala	Phe	Ala	Lys	His	Gly	
						230			235			240				
gca	cgt	agg	gac	cga	ctt	acc	aga	gct	atc	atg	gaa	gag	cac	aca	ata	824
Ala	Arg	Arg	Asp	Arg	Leu	Thr	Arg	Ala	Ile	Met	Glu	Glu	His	Thr	Ile	
						245			250			255				
gcc	cgt	aaa	aag	agt	ggt	gga	gcc	caa	caa	cat	ttc	gtg	gat	gca	ttg	872
Ala	Arg	Lys	Lys	Ser	Gly	Gly	Ala	Gln	Gln	His	Phe	Val	Asp	Ala	Leu	
						260			265			270			275	
ctc	acc	cta	caa	gag	aaa	tat	gac	ctt	agc	gag	gac	act	att	att	ggg	920
Leu	Thr	Leu	Gln	Glu	Lys	Tyr	Asp	Leu	Ser	Glu	Asp	Thr	Ile	Ile	Gly	
						280			285			290				
ctc	ctt	tgg	gat	atg	atc	act	gca	ggc	atg	gac	aca	acc	gca	atc	tct	968
Leu	Leu	Trp	Asp	Met	Ile	Thr	Ala	Gly	Met	Asp	Thr	Thr	Ala	Ile	Ser	
						295			300			305				
gtc	gaa	tgg	gcc	atg	gcc	gag	tta	att	aag	aac	cca	agg	gtg	caa	caa	1016
Val	Glu	Trp	Ala	Met	Ala	Glu	Leu	Ile	Lys	Asn	Pro	Arg	Val	Gln	Gln	
						310			315			320				
aaa	gct	caa	gag	gag	cta	gac	aat	gta	ctt	ggg	tcc	gaa	cgt	gtc	ctg	1064
Lys	Ala	Gln	Glu	Glu	Leu	Asp	Asn	Val	Leu	Gly	Ser	Glu	Arg	Val	Leu	
						325			330			335				

Fig. 4B

SEQ ID 1

acc gaa ttg gac ttc tca agc ctc cct tat cta caa tgt gta gcc aag	1112
Thr Glu Leu Asp Phe Ser Ser Leu Pro Tyr Leu Gln Cys Val Ala Lys	
340 345 350 355	
gag gca cta agg ctg cac cct cca aca cca cta atg ctc cct cat cgc	1160
Glu Ala Leu Arg Leu His Pro Pro Thr Pro Leu Met Leu Pro His Arg	
360 365 370	
gcc aat gcc aac gtc aaa att ggt ggc tac gac atc cct aag gga tca	1208
Ala Asn Ala Asn Val Lys Ile Gly Gly Tyr Asp Ile Pro Lys Gly Ser	
375 380 385	
aat gtt cat gta aat gtc tgg gcc gtg gct cgt gat cca gca gtg tgg	1256
Asn Val His Val Asn Val Trp Ala Val Ala Arg Asp Pro Ala Val Trp	
390 395 400	
cgt gac cca cta gag ttt cga ccg gaa cgg ttc tct gaa gac gat gtc	1304
Arg Asp Pro Leu Glu Phe Arg Pro Glu Arg Phe Ser Glu Asp Asp Val	
405 410 415	
gac atg aaa ggt cac gat tat agg cta ctg ccg ttt ggt gca ggg agg	1352
Asp Met Lys Gly His Asp Tyr Arg Leu Leu Pro Phe Gly Ala Gly Arg	
420 425 430 435	
cgt gtt tgc ccc ggt gca caa ctt ggc atc aat ttg gtc aca tcc atg	1400
Arg Val Cys Pro Gly Ala Gln Leu Gly Ile Asn Leu Val Thr Ser Met	
440 445 450	
atg ggt cac cta ttg cac cat ttc tat tgg agc cct cct aaa ggt gta	1448
Met Gly His Leu Leu His His Phe Tyr Trp Ser Pro Pro Lys Gly Val	
455 460 465	
aaa cca gag gag att gac atg tca gag aat cca gga ttg gtc acc tac	1496
Lys Pro Glu Glu Ile Asp Met Ser Glu Asn Pro Gly Leu Val Thr Tyr	
470 475 480	
atg cga acc ccg gtg caa gct gtt ccc act cca agg ctg cct gct cac	1544
Met Arg Thr Pro Val Gln Ala Val Pro Thr Pro Arg Leu Pro Ala His	
485 490 495	
ttg tac aaa cgt gta gct gtg gat atg taattcttag ttgttattta	1591
Leu Tyr Lys Arg Val Ala Val Asp Met	
500 505	

Fig. 4C

SEQ ID 1

ttcatgctct taaggtttg gactttgaac ttatgatgag atttgtaaaa ttccaagtga 1651

tcaaatgaag aaaagaccaa ataaaaaggc ttgacgattt aaaaaaaaaa aaaaaaaaa 1708

Fig. 4D

SEQ ID 2

Met Ala Phe Leu Leu Ile Pro Ile Ser Ile Ile Phe Ile Val Leu Ala
1 5 10 15

Tyr Gln Leu Tyr Gln Arg Leu Arg Phe Lys Leu Pro Pro Gly Pro Arg
20 25 30

Pro Trp Pro Ile Val Gly Asn Leu Tyr Asp Ile Lys Pro Val Arg Phe
35 40 45

Arg Cys Phe Ala Glu Trp Ser Gln Ala Tyr Gly Pro Ile Ile Ser Val
50 55 60

Trp Phe Gly Ser Thr Leu Asn Val Ile Val Ser Asn Ser Glu Leu Ala
65 70 75 80

Lys Glu Val Leu Lys Glu Lys Asp Gln Gln Leu Ala Asp Arg His Arg
85 90 95

Ser Arg Ser Ala Ala Lys Phe Ser Arg Asp Gly Gln Asp Leu Ile Trp
100 105 110

Ala Asp Tyr Gly Pro His Tyr Val Lys Val Thr Lys Val Cys Thr Leu
115 120 125

Glu Leu Phe Thr Pro Lys Arg Leu Glu Ala Leu Arg Pro Ile Arg Glu
130 135 140

Asp Glu Val Thr Ala Met Val Glu Ser Ile Phe Asn Asp Thr Ala Asn
145 150 155 160

Pro Glu Asn Tyr Gly Lys Ser Met Leu Val Lys Lys Tyr Leu Gly Ala
165 170 175

Val Ala Phe Asn Asn Ile Thr Arg Leu Ala Phe Gly Lys Arg Phe Val
180 185 190

Asn Ser Glu Gly Val Met Asp Glu Gln Gly Leu Glu Phe Lys Glu Ile
195 200 205

Val Ala Asn Gly Leu Lys Leu Gly Ala Ser Leu Ala Met Ala Glu His
210 215 220

Ile Pro Trp Leu Arg Trp Met Phe Pro Leu Glu Glu Gly Ala Phe Ala
225 230 235 240

Fig. 4E

SEQ ID 2

Lys His Gly Ala Arg Arg Asp Arg Leu Thr Arg Ala Ile Met Glu Glu
245 250 255

His Thr Ile Ala Arg Lys Lys Ser Gly Gly Ala Gln Gln His Phe Val
260 265 270

Asp Ala Leu Leu Thr Leu Gln Glu Lys Tyr Asp Leu Ser Glu Asp Thr
275 280 285

Ile Ile Gly Leu Leu Trp Asp Met Ile Thr Ala Gly Met Asp Thr Thr
290 295 300

Ala Ile Ser Val Glu Trp Ala Met Ala Glu Leu Ile Lys Asn Pro Arg
305 310 315 320

Val Gln Gln Lys Ala Gln Glu Glu Leu Asp Asn Val Leu Gly Ser Glu
325 330 335

Arg Val Leu Thr Glu Leu Asp Phe Ser Ser Leu Pro Tyr Leu Gln Cys
340 345 350

Val Ala Lys Glu Ala Leu Arg Leu His Pro Pro Thr Pro Leu Met Leu
355 360 365

Pro His Arg Ala Asn Ala Asn Val Lys Ile Gly Gly Tyr Asp Ile Pro
370 375 380

Lys Gly Ser Asn Val His Val Asn Val Trp Ala Val Ala Arg Asp Pro
385 390 395 400

Ala Val Trp Arg Asp Pro Leu Glu Phe Arg Pro Glu Arg Phe Ser Glu
405 410 415

Asp Asp Val Asp Met Lys Gly His Asp Tyr Arg Leu Leu Pro Phe Gly
420 425 430

Ala Gly Arg Arg Val Cys Pro Gly Ala Gln Leu Gly Ile Asn Leu Val
435 440 445

Thr Ser Met Met Gly His Leu Leu His His Phe Tyr Trp Ser Pro Pro
450 455 460

Lys Gly Val Lys Pro Glu Glu Ile Asp Met Ser Glu Asn Pro Gly Leu
465 470 475 480

Fig. 4F

SEQ ID 2

Val Thr Tyr Met Arg Thr Pro Val Gln Ala Val Pro Thr Pro Arg Leu
485 490 495

Pro Ala His Leu Tyr Lys Arg Val Ala Val Asp Met
500 505

Fig. 4G

SEQ ID 3

<400> 3
tgcaaacctg cacaacacaaa gagagagaag aagaaaaagg aagagaggag agagagagag 60

agagagagaa gcc atg gat tct tct cat gaa gcc ttg caa cca cta 109
Met Asp Ser Ser Leu His Glu Ala Leu Gln Pro Leu
1 5 10

ccc atg acg ctg ttc ttc att ata cct ttg cta ctc tta ttg ggc cta 157
Pro Met Thr Leu Phe Phe Ile Ile Pro Leu Leu Leu Leu Gly Leu
15 20 25

gta tct cgg ctt cgc cag aga cta cca tac cca cca ggc cca aaa ggc 205
Val Ser Arg Leu Arg Gln Arg Leu Pro Tyr Pro Pro Gly Pro Lys Gly
30 35 40

tta ccg gtg atc gga aac atg ctc atg gat caa ctc act cac cga 253
Leu Pro Val Ile Gly Asn Met Leu Met Met Asp Gln Leu Thr His Arg
45 50 55 60

gga ctc gcc aaa ctc gcc aaa caa tac ggt cta ttc cac ctc aag 301
Gly Leu Ala Lys Leu Ala Lys Gln Tyr Gly Leu Phe His Leu Lys
65 70 75

atg gga ttc tta cac atg gtg gcc gtt tcc aca ccc gac atg gct cgc 349
Met Gly Phe Leu His Met Val Ala Val Ser Thr Pro Asp Met Ala Arg
80 85 90

caa gtc ctt caa gtc caa gac aac atc ttc tcg aac cgg cca gcc acc 397
Gln Val Leu Gln Val Gln Asp Asn Ile Phe Ser Asn Arg Pro Ala Thr
95 100 105

ata gcc atc agc tac ctc acc tat gac cga gcc gac atg gcc ttc gct 445
Ile Ala Ile Ser Tyr Leu Thr Tyr Asp Arg Ala Asp Met Ala Phe Ala
110 115 120

cac tac ggc ccg ttt tgg cgt cag atg cgt aaa ctc tgc gtc atg aaa 493
His Tyr Gly Pro Phe Trp Arg Gln Met Arg Lys Leu Cys Val Met Lys
125 130 135 140

tta ttt agc cgg aaa cga gcc gag tcg tgg gag tcg gtc cga gac gag 541
Leu Phe Ser Arg Lys Arg Ala Glu Ser Trp Glu Ser Val Arg Asp Glu
145 150 155

gtc gac tcg gca gta cga gtg gtc gcg tcc aat att ggg tcg acg gtg 589
Val Asp Ser Ala Val Arg Val Ala Ser Asn Ile Gly Ser Thr Val
160 165 170

Fig. 5A

SEQ ID 3

aat atc ggc gag ctg gtt ttt gct ctg acg aag aat att act tac agg	637		
Asn Ile Gly Glu Leu Val Phe Ala Leu Thr Lys Asn Ile Thr Tyr Arg			
175	180	185	
gcg gct ttt ggg acg atc tcg cat gag gac cag gag ttc gtg gcc	685		
Ala Ala Phe Gly Thr Ile Ser His Glu Asp Gln Asp Glu Phe Val Ala			
190	195	200	
ata ctg caa gag ttt tcg cag ctg ttt ggt gct ttt aat ata gct gat	733		
Ile Leu Gln Glu Phe Ser Gln Leu Phe Gly Ala Phe Asn Ile Ala Asp			
205	210	215	220
ttt atc cct tgg ctc aaa tgg gtt cct cag ggg att aac gtc agg ctc	781		
Phe Ile Pro Trp Leu Lys Trp Val Pro Gln Gly Ile Asn Val Arg Leu			
225	230	235	
aac aag gca cga ggg gcg ctt gat ggg ttt att gac aag atc atc gac	829		
Asn Lys Ala Arg Gly Ala Leu Asp Gly Phe Ile Asp Lys Ile Ile Asp			
240	245	250	
gat cat ata cag aag ggg agt aaa aac tcg gag gag gtt gat act gat	877		
Asp His Ile Gln Lys Gly Ser Lys Asn Ser Glu Glu Val Asp Thr Asp			
255	260	265	
atg gta gat gat tta ctt gct ttt tac ggt gag gaa gcc aaa gta agc	925		
Met Val Asp Asp Leu Leu Ala Phe Tyr Gly Glu Ala Lys Val Ser			
270	275	280	
gaa tct gac gat ctt caa aat tcc atc aaa ctc acc aaa gac aac atc	973		
Glu Ser Asp Asp Leu Gln Asn Ser Ile Lys Leu Thr Lys Asp Asn Ile			
285	290	295	300
aaa gct atc atg gac gta atg ttt gga ggg acc gaa acg gtg gcg tcc	1021		
Lys Ala Ile Met Asp Val Met Phe Gly Gly Thr Glu Thr Val Ala Ser			
305	310	315	
gcg att gaa tgg gcc atg acg gag ctg atg aaa agc cca gaa gat cta	1069		
Ala Ile Glu Trp Ala Met Thr Glu Leu Met Lys Ser Pro Glu Asp Leu			
320	325	330	
aag aag gtc caa caa gaa ctc gcc gtg gtg gtg ggt ctt gac cgg cga	1117		
Lys Lys Val Gln Gln Glu Leu Ala Val Val Gly Leu Asp Arg Arg			
335	340	345	

Fig. 5B

SEQ ID 3

gtc gaa gag aaa gac ttc gag aag ctc acc tac ttg ...a tgc gta ctg	1165		
Val Glu Glu Lys Asp Phe Glu Lys Leu Thr Tyr Leu Lys Cys Val Leu			
350	355	360	
aag gaa gtc ctt cgc ctc cac cca ccc atc cca ctc ctc ctc cac gag	1213		
Lys Glu Val Leu Arg Leu His Pro Pro Ile Pro Leu Leu Leu His Glu			
365	370	375	380
act gcc gag gac gcc gag gtc ggc ggc tac tac att ccg gcg aaa tcg	1261		
Thr Ala Glu Asp Ala Glu Val Gly Gly Tyr Tyr Ile Pro Ala Lys Ser			
385	390	395	
cgg gtg atg atc aac gcg tgc gcc atc ggc cg ^g gac aag aac tcg tgg	1309		
Arg Val Met Ile Asn Ala Cys Ala Ile Gly Arg Asp Lys Asn Ser Trp			
400	405	410	
gcc gac cca gat acg ttt agg ccc tcc agg ttt ctc aaa gac ggt gtg	1357		
Ala Asp Pro Asp Thr Phe Arg Pro Ser Arg Phe Leu Lys Asp Gly Val			
415	420	425	
ccc gat ttc aaa ggg aac aac ttc gag ttc atc cca ttc ggg tca ggt	1405		
Pro Asp Phe Lys Gly Asn Asn Phe Glu Phe Ile Pro Phe Gly Ser Gly			
430	435	440	
cgt cg ^g tct tgc ccc ggt atg caa ctc gga ctc tac gcg cta gag acg	1453		
Arg Arg Ser Cys Pro Gly Met Gln Leu Gly Leu Tyr Ala Leu Glu Thr			
445	450	455	460
act gtg gct cac ctc ctt cac tgt ttc acg tgg gag ttg ccg gac ggg	1501		
Thr Val Ala His Leu Leu His Cys Phe Thr Trp Glu Leu Pro Asp Gly			
465	470	475	
atg aaa ccg agt gaa ctc gag atg aat gat gtg ttt gga ctc acc gcg	1549		
Met Lys Pro Ser Glu Leu Glu Met Asn Asp Val Phe Gly Leu Thr Ala			
480	485	490	
cca aga gcg att cga ctc acc gcc gtg ccg agt cca cgc ctt ctc tgt	1597		
Pro Arg Ala Ile Arg Leu Thr Ala Val Pro Ser Pro Arg Leu Leu Cys			
495	500	505	
cct ctc tat tgatcgaatg attggggag ctttggag gggctttat	1646		
Pro Leu Tyr			
510			

Fig. 5C

SEQ ID 3

ggagactcta tatatacatg ggaagtgaaa caacgacagg tgaatgcttg gatTTTgg 1706
atataattggg gagggagggg aaaaaaaaaa taatgaaagg aaagaaaaaga gagaatttga 1766
atTTCTCTTC ctctgtggat aaaagcctcg ttttaattt ttttatgtg gagatattt 1826
tgtttgtta ttttatctc ttttttgca ataacactca aaaataaaaa aaaaaaa 1883

Fig. 5D

SEQ ID 4

<400> 4
Met Asp Ser Ser Leu His Glu Ala Leu Gln Pro Leu Pro Met Thr Leu
1 5 10 15
Phe Phe Ile Ile Pro Leu Leu Leu Leu Gly Leu Val Ser Arg Leu
20 25 30
Arg Gln Arg Leu Pro Tyr Pro Pro Gly Pro Lys Gly Leu Pro Val Ile
35 40 45
Gly Asn Met Leu Met Met Asp Gln Leu Thr His Arg Gly Leu Ala Lys
50 55 60
Leu Ala Lys Gln Tyr Gly Gly Leu Phe His Leu Lys Met Gly Phe Leu
65 70 75 80
His Met Val Ala Val Ser Thr Pro Asp Met Ala Arg Gln Val Leu Gln
85 90 95
Val Gln Asp Asn Ile Phe Ser Asn Arg Pro Ala Thr Ile Ala Ile Ser
100 105 110
Tyr Leu Thr Tyr Asp Arg Ala Asp Met Ala Phe Ala His Tyr Gly Pro
115 120 125
Phe Trp Arg Gln Met Arg Lys Leu Cys Val Met Lys Leu Phe Ser Arg
130 135 140
Lys Arg Ala Glu Ser Trp Glu Ser Val Arg Asp Glu Val Asp Ser Ala
145 150 155 160
Val Arg Val Val Ala Ser Asn Ile Gly Ser Thr Val Asn Ile Gly Glu
165 170 175
Leu Val Phe Ala Leu Thr Lys Asn Ile Thr Tyr Arg Ala Ala Phe Gly
180 185 190
Thr Ile Ser His Glu Asp Gln Asp Glu Phe Val Ala Ile Leu Gln Glu
195 200 205
Phe Ser Gln Leu Phe Gly Ala Phe Asn Ile Ala Asp Phe Ile Pro Trp
210 215 220
Leu Lys Trp Val Pro Gln Gly Ile Asn Val Arg Leu Asn Lys Ala Arg
225 230 235 240

Fig. 5E

SEQ ID 4

Gly Ala Leu Asp Gly Phe Ile Asp Lys Ile Ile Asp Asp His Ile Gln
245 250 255

Lys Gly Ser Lys Asn Ser Glu Glu Val Asp Thr Asp Met Val Asp Asp
260 265 270

Leu Leu Ala Phe Tyr Gly Glu Glu Ala Lys Val Ser Glu Ser Asp Asp
275 280 285

Leu Gln Asn Ser Ile Lys Leu Thr Lys Asp Asn Ile Lys Ala Ile Met
290 295 300

Asp Val Met Phe Gly Gly Thr Glu Thr Val Ala Ser Ala Ile Glu Trp
305 310 315 320

Ala Met Thr Glu Leu Met Lys Ser Pro Glu Asp Leu Lys Lys Val Gln
325 330 335

Gln Glu Leu Ala Val Val Val Gly Leu Asp Arg Arg Val Glu Glu Lys
340 345 350

Asp Phe Glu Lys Leu Thr Tyr Leu Lys Cys Val Leu Lys Glu Val Leu
355 360 365

Arg Leu His Pro Pro Ile Pro Leu Leu Leu His Glu Thr Ala Glu Asp
370 375 380

Ala Glu Val Gly Gly Tyr Tyr Ile Pro Ala Lys Ser Arg Val Met Ile
385 390 395 400

Asn Ala Cys Ala Ile Gly Arg Asp Lys Asn Ser Trp Ala Asp Pro Asp
405 410 415

Thr Phe Arg Pro Ser Arg Phe Leu Lys Asp Gly Val Pro Asp Phe Lys
420 425 430

Gly Asn Asn Phe Glu Phe Ile Pro Phe Gly Ser Gly Arg Arg Ser Cys
435 440 445

Pro Gly Met Gln Leu Gly Leu Tyr Ala Leu Glu Thr Thr Val Ala His
450 455 460

Leu Leu His Cys Phe Thr Trp Glu Leu Pro Asp Gly Met Lys Pro Ser
465 470 475 480

SEQ ID 4

Glu Leu Glu Met Asn Asp Val Phe Gly Leu Thr Ala Pro Arg Ala Ile
485 490 495

Arg Leu Thr Ala Val Pro Ser Pro Arg Leu Leu Cys Pro Leu Tyr
500 505 510

Fig. 5G

SEQ ID 10

<400> 10
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ttattgtaat ctaaccaatt ctaatttcca ccctgggtgtg aactgactga caaatgcggt 120
ccgaaaacag cgaatgaaat gtctgggtga tcggtcaaac aagcggtggg cgagagagcg 180
cggtgttgg cctagccggg atggggtag gtagacggcg tattaccggc gagttgtccg 240
aatggagttt tcggggtagg tagtaacgta gacgtcaatg gaaaaagtca taatctccgt 300
caaaaatcca accgctcctt cacatcgca agttggtggc cacgggaccc tccacccact 360
cactcaatcg atcgccctgcc gtgggtgccc attattcaac catacgccac ttgactcttc 420
accaacaatt ccaggccggc tttctataca atgtactgca caggaaaatc caatataaaa 480
agccggcctc tgcttccttc tca tagtagccc ccagctcatt caattcttcc cactgcaggc 540
tacatttgtc agacacgttt tccgcccattt ttccgcctgtt tctgcggaga atttgatcag 600
gttcggattt ggatttgaatc aattgaaagg tttttatattt cagtatttcg atcgccatg 659

Fig. 6

SEQ ID 11

<400> 11
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aaagaaaaca aaattttcat cttaacata attataattg tgttcacaaa attcaaactt 120
aaacccttaa tataaagaat ttcttcAAC aatacacttt aatcacaact tcttcaatca 180
caacctcgtc caacaaaatt aaaatagatt aataaataaa taaacttaac tatttaaaaa 240
aaaatattat acaaaattta taaaacttc aaaataaaca aactttttat acaaaattca 300
tcaaaacttt aaaataaAGC taaacactga aatgtgagt acattttaaa ggacgctgat 360
cacaaaaatt ttgaaaacat aaacaaactt gaaactctac ctttaagaa tgagttgtc 420
gtctcattaa ctcattagtt ttatagttcg aatccaatta acgtatctt tattttatgg 480
aataagggtg ttttaataag tgattttggg attttttag taatttattt gtgatatgtt 540
atggagttt taaaaatata tataatata tatatttttg gttgagttt actaaaaatl 600
tggaaaaggt tggtaagaac tataaattga gttgtgaatg agtgtttat ggattttta 660
agatgtlaaa tttatataatg taattaaaat tttatTTGA ataacaaaaa ttataattgg 720
ataaaaaattt gttttgttaa atttagatg aaaatttcaa aatctaaaat aattaaacac 780
tattttttt aaaaaatttgg tggtaattt ttatctata ttaagttaa aatttagaaa 840
aaattaattt taaattaata aacttttggaa gtcaaattt ccaaattt tccaaatata 900
taaatctatt ttgcattcaa aatacaattt aaataataaa acttcatggg atagattttt 960
caatttgtat aaaaaccaa aatctcaaattt aaaatttaaa ttacaaaaca ttatcaacat 1020
tatgatttca agaaagacaa taaccagttt ccaataaaaat aaaaaacctc atggcccgta 1080
attaagatct cattaattaa ttcttatttt ttaattttt tacatagaaa atatctttat 1140
attgtatcca agaaatataag aatgttctcg tccaggactt attaatctcc aaacaagttt 1200
caaaatcatt acattaaAGC tcatcatgtc atttggat tggaaattt attgtataag 1260
agaaatataag aatgttctcg tctaggactt attaatctcc aaacaatattt caaaatcatt 1320

Fig. 7A

SEQ ID 11

acattaaagc tcatcatgtc atttgtggat tggaaattag aaaaaaaaaa tcccaaatat 1380
ttctctcaat ctcccaaaat atagttcgaa ctccatattt ttggaaattg agaatttttt 1440
tacccaataa tatattttt tatacattt agagatttc cagacatatt tgctctggga 1500
tttattggaa tgaagggtga gttataaact ttcagtaatc caagtatctt cggttttga 1560
agatactaaa tccattatataataaaaaaca cattttaaac accaattaa tggatttca 1620
gatttgtatc ccatgctatt ggctaaggca tttttcttat tgtaatctaa ccaattctaa 1680
tttccacccct ggtgtgaact gactgacaaa tgcggccga aaacagcgaa tgaatgtct 1740
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ggtaggttag acggcgattt accggcgagt tgcgttgcgagttttcggttagt 1860
aacgttagacg tcaatggaaa aagtataat ctccgtcaaa aatccaaccg ctccttcaca 1920
tcgcagagtt ggtggccacg ggaccctcca cccactcaact cgatcgccctg ccgtgggtgc 1980
ccattattca accatacgcc acttgactct tcaccaacaa ttccaggccg gctttctata 2040
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ccccagctca ttcaattctt cccactgcag gctacatttgcagacacgt ttccggcat 2160
tttgcctg tttctgcgga gaatttgcgttgcgat tggattgaa tcaattgaaa 2220
ggtttttattt ttcaattttt cgatcgccat g 2251

Fig. 7B

SEQ ID 9

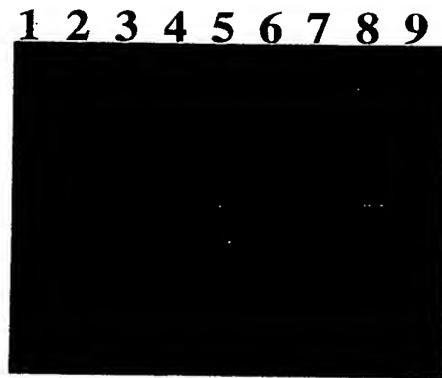
<400> 9
aaagataata tatgtgtatg cctactacta cacattgtt tgaagtgtgt aaacatagt 60
caacactagg aggactcaca atgagcactt gttgacatga aactagctaa atgccaaca 120
atai :agtga aagctagttt aactaaccctt tttgactttc aqatgatat atttatatcc 180
ctactacgtc ttcccttttt tgcctttctc ttgtgattaa accttccttg aaacaattct 240
caaatgtaaa attaaacctt gaaacttgtt gagacccaaac ttcccttagga gaaaccacat 300
ttatgacaac atatatacac caacccattt catactataa tatttggattt acctgcagcg 360
aacgaaagaa acgctgtctc accaactcgt gcactacatc ccgaaactta accttcccct 420
gatacagattt gaagagccga aaaaagcgtg catccaaattt tctggatgg tgaggagccg 480
aaaaacgcgt gcgcctaattt ttttgagat gggccggaaa ataatgcgtg catctaaattt 540
ttcacgtgtc gcgttatttgc gaggttgcgc tgaatgtat cctgtgcgtg agccacattc 600
attccattgg ttgaccgcgc ggtaccgcga ggaccgtggg gtctcacaga tacgcggatg 660
gtggatcagc actgagaaga ttagatgtatc accaggcggg catttgaagt aaaaacttgg 720
gggtggttgg caagtacgcg acaaagaggg gtatgcgcgca aggaagcggag ttggatgcaa 780
ataatattac aaagtgggtt ggtgggcattt agcatcaacc agaatgtatgt tggatgtt 840
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aacacatacc tttaactaat aaaaataccctt ctaacaaataa cggaaacgaa tgagttatca 1020
cagaccccttca actaataaga tagccatcag acccacatctt cctgactgac caaaaacaaa 1080
tgacttcaac caactaagat acccatcaaa gcttacccac aacccaaattt ctcacttccc 1140
cttaccagac caaccaagca gacccatcag acccacatctt cctgactgac caaaaacaaa 1200
gtgccaccgt tgaagaatgg cactcagggtt tggtaatccc tccacgtgtt tggatgtt 1260
gtttgggttggaa gacggcgtgtt tggatgttcc accttccagggtt tggagaaca agggaaattgg 1320

Fig. 8A

SEQ ID 9

gcttatatta ggcctggatc tcttgtttca gagcaggagt agttcaggac aggaactagc 1380
attcaagaat tcaattgccc tgccctgctc tgctctgctt tgctcaactt attgatccct 1440
gctctggttt gttcaatttc ttgacccctg ctgggttctg ctctggtttg cacactttct 1500
cgattatata agtcatttg gatccttgca aggaagagaa tatg 1544

Fig. 8B



Lanes 1-4: PCR amplification of Sweetgum P450-1 gene from control and transgenic loblolly pine cell lines. Note the 600 bp amplified fragment in lanes 2-4.

Lanes 6-9: PCR amplification of Hygromycin gene from control and transgenic loblolly pine cell lines. Note the 1000 bp amplified fragment in lanes 7-9.

Lane 1: Control PT52 line

Lane 2: Transgenic line Y2

Lane 3: Transgenic line Y17

Lane 4: Control plasmid pSSLsP450-1-iml-s

Lane 5: DNA size marker Phi 174/HaeII (BRL); top 4 bands indicate molecular size of 1354, 1078, 872 and 603 bp.

Lane 6: Control PT52 line

Lane 7: Transgenic line Y7

Lane 8: Transgenic line O4

Lane 9: Control plasmid pHygro

FIG. 9